

CRF Processing Date: 5/13/02  
Edited by: DC  
Verified by: (STIC staff)

Serial Number: 10/039,050

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line: #3
- ☐ Edited a format error in the Current Application Data section, specifically: ENTERED
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: \_\_\_\_\_
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: \_\_\_\_\_
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: \_\_\_\_\_
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: \_\_\_\_\_
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: \_\_\_\_\_
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file;  
☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_
- ☐ Inserted mandatory headings, specifically: \_\_\_\_\_
- ☐ Corrected an obvious error in the response, specifically: \_\_\_\_\_
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: \_\_\_\_\_
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_
- ☐ Other: \_\_\_\_\_

\*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95



OIPE

## RAW SEQUENCE LISTING

DATE: 05/13/2002

PATENT APPLICATION: US/10/039,050

TIME: 16:48:28

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Output Set: N:\CRF3\05132002\J039050.raw

4 <110> APPLICANT: Autogen Research Pty Ltd

6 <120> TITLE OF INVENTION: Novel genes and their use in the modulation of obesity, diabetes

7 and energy imbalance

11 <130> FILE REFERENCE: 2309315/TDO

14 <140> CURRENT APPLICATION NUMBER: 10/039,050

C--> 15 <141> CURRENT FILING DATE: 2002-04-25

18 <150> PRIOR APPLICATION NUMBER: 60/141,441

19 <151> PRIOR FILING DATE: 1999-06-29

23 <160> NUMBER OF SEQ ID NOS: 22

26 <170> SOFTWARE: PatentIn Ver. 2.0

29 <210> SEQ ID NO: 1

30 <211> LENGTH: 1669

31 <212> TYPE: DNA

32 <213> ORGANISM: mammalian

35 <220> FEATURE:

36 <221> NAME/KEY: CDS

37 <222> LOCATION: (43)..(1104)

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43 Met Cys Phe Trp

44 1

46 ggg ata ttt ttg tgt ttg atc ttc ctg gag aaa agt tgg gga cag ata 102

47 Gly Ile Phe Leu Cys Leu Ile Phe Leu Glu Lys Ser Trp Gly Gln Ile

48 5 10 15 20

50 caa atg tcg tgt tgg ccc aag cct ttg att cca gaa ctt gag agg cag 150

51 Gln Met Ser Cys Trp Pro Lys Pro Leu Ile Pro Glu Leu Glu Arg Gln

52 25 30 35

54 aga tgc acc gtt gta aca cca aaa gtc ttc cga gtc gga gaa tat gaa 198

55 Arg Cys Thr Val Val Thr Pro Lys Val Phe Arg Val Gly Glu Tyr Glu

56 40 45 50

58 caa gtt aca ttt gaa gcc cac ggt cac act gac cca ttt gat gta acc 246

59 Gln Val Thr Phe Glu Ala His Gly His Thr Asp Pro Phe Asp Val Thr

60 55 60 65

61 atc tct ata aaa agt tac cct gat aaa aat gct aat tac tct tca agc 294

62 Ile Ser Ile Lys Ser Tyr Pro Asp Lys Asn Ala Asn Tyr Ser Ser Ser

63 70 75 80

65 tct gta cat tta tca cca gaa aat aaa ttc aaa aac tct aca atc tta 342

66 Ser Val His Leu Ser Pro Glu Asn Lys Phe Lys Asn Ser Thr Ile Leu

67 85 90 95 100

69 aca att cag ccc aaa cag ttg tct gaa ggg caa aac tcg tct tcg cat 390

70 Thr Ile Gln Pro Lys Gln Leu Ser Glu Gly Gln Asn Ser Ser Ser His

71 105 110 115

73 gtg tat ttg gaa gtt gtg tcc aag cat ttt tca aca tca aaa ata atg 438

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78 Ser Ile Val Tyr Asp Asn Gly Thr Leu Phe Ile Gln Thr Asp Lys Pro
79          135          140          145
81 gtg tac act cca gag cag cct gta aag gtt gcc gtg tat tcg ctg gat 534
82 Val Tyr Thr Pro Glu Gln Pro Val Lys Val Ala Val Tyr Ser Leu Asp
83          150          155          160
85 gaa gcc tta aag cca gtc acc aga gag aca gtc tta acg ttc ata gac 582
86 Glu Ala Leu Lys Pro Val Thr Arg Glu Thr Val Leu Thr Phe Ile Asp
87 165          170          175          180
89 cct gaa gga tcc gaa gtt ggc ata gta gaa gga agc aat cat act gga 630
90 Pro Glu Gly Ser Glu Val Gly Ile Val Glu Gly Ser Asn His Thr Gly
91          185          190          195
93 atc acc tct ttc cct gac ttc agg att cct act aac cct aag ccc ggt 678
94 Ile Thr Ser Phe Pro Asp Phe Arg Ile Pro Thr Asn Pro Lys Pro Gly
95          200          205          210
97 aga tgg atg atc aag gct aaa tat aga gaa gat gct tca aca gct gga 726
98 Arg Trp Met Ile Lys Ala Lys Tyr Arg Glu Asp Ala Ser Thr Ala Gly
99          215          220          225
101 acc aca cac ttt gaa att aaa gag cat gat aaa gct ttc aaa ata gcc 774
102 Thr Thr His Phe Glu Ile Lys Glu His Asp Lys Ala Phe Lys Ile Ala
103          230          235          240
105 ctc gtt cca aca agt gat ctg gaa cac cca atg gaa gaa gca cgt ggc 822
106 Leu Val Pro Thr Ser Asp Leu Glu His Pro Met Glu Glu Ala Arg Gly
107 245          250          255          260
109 ctg agt ctc cag cca aaa aag tcc ctg caa gag atg ata cat gag caa 870
110 Leu Ser Leu Gln Pro Lys Lys Ser Leu Gln Glu Met Ile His Glu Gln
111          265          270          275
113 gct tcg aaa tac aaa cat cca gta ctg aag aaa tgt tgt tat gat gga 918
115 Ala Ser Lys Tyr Lys His Pro Val Leu Lys Lys Cys Cys Tyr Asp Gly
116          280          285          290
118 gcc aga tat aac cac cat gaa acc tgt gag gaa cga gtt gcc cgt gtg 966
119 Ala Arg Tyr Asn His His Glu Thr Cys Glu Glu Arg Val Ala Arg Val
120          295          300          305
122 aaa ata ggc cca aac tgt gtc aga gcc ttc agt gaa tgc tgt gcc ctg 1014
123 Lys Ile Gly Pro Asn Cys Val Arg Ala Phe Ser Glu Cys Cys Ala Leu
124          310          315          320
126 gct agc gag aat acc ttt aag aat atc ctc atg tcg cgt ccc gat gac 1062
127 Ala Ser Glu Asn Thr Phe Lys Asn Ile Leu Met Ser Arg Pro Asp Asp
128 325          330          335          340
130 agt gga tat ttt act tta tct gct acc ata ctg gaa aat gct taa 1107
131 Ser Gly Tyr Phe Thr Leu Ser Ala Thr Ile Leu Glu Asn Ala
132          345          350
134 tcttattccc tgcaagtatt tgaagattac aagtattttc tgtgccttca cttttgctgg 1167
136 aaactaatgc acaaaatcaa acggagttca tacagcagtg aagcccttcc gctgtaactt 1227
138 tgccataaat agccttggtc gcacggaggt catttcataa ccgtaattta tccactggtc 1287
140 tcacaagtga gaccaagctg ataaaaacaa attcaccaga agagtttgat tgccatgctc 1347
142 agtgaccttg cccatcttcc tgtcaggacc ctcggtgccc taacatagta gaggggtgctc 1407

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146 cagcacacac cgtgtgggcc accgtgctgc ccaggtgtcc ataatgctac actaagtcgc 1527
148 cacgaataat cagttgtgcc agcagagtat gggagccgct aaaggatact atgcttgtaa 1587
150 atgtgtatca caatcagaat gtttaaataca ataaaatagt attgcccgcg ttaaaaaaaaa 1647
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156 <211> LENGTH: 354
157 <212> TYPE: PRT
158 <213> ORGANISM: mammalian
160 <400> SEQUENCE: 2
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162   1           5           10           15
164 Trp Gly Gln Ile Gln Met Ser Cys Trp Pro Lys Pro Leu Ile Pro Glu
165           20           25           30
167 Leu Glu Arg Gln Arg Cys Thr Val Val Thr Pro Lys Val Phe Arg Val
168           35           40           45
170 Gly Glu Tyr Glu Gln Val Thr Phe Glu Ala His Gly His Thr Asp Pro
171           50           55           60
173 Phe Asp Val Thr Ile Ser Ile Lys Ser Tyr Pro Asp Lys Asn Ala Asn
174   65           70           75           80
176 Tyr Ser Ser Ser Ser Val His Leu Ser Pro Glu Asn Lys Phe Lys Asn
177           85           90           95
179 Ser Thr Ile Leu Thr Ile Gln Pro Lys Gln Leu Ser Glu Gly Gln Asn
180           100          105          110
182 Ser Ser Ser His Val Tyr Leu Glu Val Val Ser Lys His Phe Ser Thr
183           115          120          125
185 Ser Lys Ile Met Ser Ile Val Tyr Asp Asn Gly Thr Leu Phe Ile Gln
186           130          135          140
188 Thr Asp Lys Pro Val Tyr Thr Pro Glu Gln Pro Val Lys Val Ala Val
189 145           150          155          160
191 Tyr Ser Leu Asp Glu Ala Leu Lys Pro Val Thr Arg Glu Thr Val Leu
192           165          170          175
195 Thr Phe Ile Asp Pro Glu Gly Ser Glu Val Gly Ile Val Glu Gly Ser
196           180          185          190
198 Asn His Thr Gly Ile Thr Ser Phe Pro Asp Phe Arg Ile Pro Thr Asn
199           195          200          205
201 Pro Lys Pro Gly Arg Trp Met Ile Lys Ala Lys Tyr Arg Glu Asp Ala
202           210          215          220
204 Ser Thr Ala Gly Thr Thr His Phe Glu Ile Lys Glu His Asp Lys Ala
205 225           230          235          240
207 Phe Lys Ile Ala Leu Val Pro Thr Ser Asp Leu Glu His Pro Met Glu
208           245          250          255
210 Glu Ala Arg Gly Leu Ser Leu Gln Pro Lys Lys Ser Leu Gln Glu Met
211           260          265          270
213 Ile His Glu Gln Ala Ser Lys Tyr Lys His Pro Val Leu Lys Lys Cys
214           275          280          285
216 Cys Tyr Asp Gly Ala Arg Tyr Asn His His Glu Thr Cys Glu Glu Arg
217           290          295          300
219 Val Ala Arg Val Lys Ile Gly Pro Asn Cys Val Arg Ala Phe Ser Glu

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220 305          310          315          320
222 Cys Cys Ala Leu Ala Ser Glu Asn Thr Phe Lys Asn Ile Leu Met Ser
223          325          330          335
225 Arg Pro Asp Asp Ser Gly Tyr Phe Thr Leu Ser Ala Thr Ile Leu Glu
226          340          345          350
228 Asn Ala
229 <210> SEQ ID NO: 3
230 <211> LENGTH: 1170
231 <212> TYPE: DNA
232 <213> ORGANISM: mammalian
234 <220> FEATURE:
235 <221> NAME/KEY: CDS
236 <222> LOCATION: (21)..(586)
238 <400> SEQUENCE: 3
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241          Met Glu Ser Ala Glu Glu Pro Leu Pro Ala Arg
242          1          5          10
244 ccg gcg ctg gag acc gag ggc ctg agg ttc ctg cac gtc aca gtg ggc 100
245 Pro Ala Leu Glu Thr Glu Gly Leu Arg Phe Leu His Val Thr Val Gly
246          15          20          25
248 tcc ctg ctg gcc agc tat ggc tgg tac gtc ctc ttc agc tgc atc ctt 148
249 Ser Leu Leu Ala Ser Tyr Gly Trp Tyr Val Leu Phe Ser Cys Ile Leu
250          30          35          40
252 ctg tac att gtc atc cag aag ctc tcc gtc cga ttg agg gtt ttg agg 196
253 Leu Tyr Ile Val Ile Gln Lys Leu Ser Val Arg Leu Arg Val Leu Arg
254          45          50          55
256 cag agg cag ctg gac cag gct gac gct gtt ctg gaa cct gat gct gtt 244
258 Gln Arg Gln Leu Asp Gln Ala Asp Ala Val Leu Glu Pro Asp Ala Val
259 60          65          70          75
261 gtt aag cga caa gag gct tta gcc gct gct cgt ttg aga atg cag gaa 292
262 Val Lys Arg Gln Glu Ala Leu Ala Ala Arg Leu Arg Met Gln Glu
263          80          85          90
265 gat cta aat gcc caa gtt gaa aag cat aag gaa aaa cta aga cag ctt 340
266 Asp Leu Asn Ala Gln Val Glu Lys His Lys Glu Lys Leu Arg Gln Leu
267          95          100          105
269 gaa gaa gaa aaa agg aga cag aag att gaa atg tgg gac agc atg caa 388
270 Glu Glu Glu Lys Arg Arg Gln Lys Ile Glu Met Trp Asp Ser Met Gln
271          110          115          120
273 gaa ggc aga agt tac aga aga aat cca gga agg cct cag gaa gaa gat 436
274 Glu Gly Arg Ser Tyr Arg Arg Asn Pro Gly Arg Pro Gln Glu Glu Asp
275          125          130          135
277 ggt cct gga cct tct act tca tca tct gtc acc cgc aaa gga aaa tct 484
278 Gly Pro Gly Pro Ser Thr Ser Ser Ser Val Thr Arg Lys Gly Lys Ser
279 140          145          150          155
281 gac aaa aag cct ttg agg gga aat ggt tat aac cct ctg acg ggt gaa 532
282 Asp Lys Lys Pro Leu Arg Gly Asn Gly Tyr Asn Pro Leu Thr Gly Glu
283          160          165          170
285 ggg ggt gga acc tgc gcc tgg aga cct gga cgc agg ggc cca tca tct 580
286 Gly Gly Gly Thr Cys Ala Trp Arg Pro Gly Arg Arg Gly Pro Ser Ser

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287          175          180          185
289 ggt gga tga agctaagacc cttgttagtg tcgctttgac attagcaagg          629
290 Gly Gly
292 tgaaccctta accctcaact cagttgcctt acgcacactt tcacagtgc tagccaagga 689
294 gaggtggggc ttatttccat tcgtagctac ctgtattcta agggctttgg tcagtgtgag 749
296 ctatggacat tgtcattagg tcatattcta cttagacaac agtcattgat ttcattggcta 809
298 cttgctagtt gatagggttaa aggcctctcg ctgttttagca aacttcataa aggaggccca 869
300 gtgatgatcc tttggggtag aagtctctgc tgacaggatg gtctctgtga caggatgcgt 929
302 tcaatgatgt cttccttata aatgggtgagc ccaccagtga ggattactga tgtgcacagt 989
304 tgatgggggtt tgcttctgta tttttatatt tatgtacaga aatttgcaaa aaaaaataaa 1049
306 aagtaacatt tttagcatct ttattaaact caaggaaatt tcgttgtgag cttgactttg 1109
308 tctatcagac attaaacagc tttttatcat taaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1169
310 a          1170

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313 &lt;210&gt; SEQ ID NO: 4

314 &lt;211&gt; LENGTH: 189

315 &lt;212&gt; TYPE: PRT

316 &lt;213&gt; ORGANISM: mammalian

318 &lt;400&gt; SEQUENCE: 4

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320 Met Glu Ser Ala Glu Glu Pro Leu Pro Ala Arg Pro Ala Leu Glu Thr
321   1          5          10          15
322 Glu Gly Leu Arg Phe Leu His Val Thr Val Gly Ser Leu Leu Ala Ser
323          20          25          30
325 Tyr Gly Trp Tyr Val Leu Phe Ser Cys Ile Leu Leu Tyr Ile Val Ile
326          35          40          45
328 Gln Lys Leu Ser Val Arg Leu Arg Val Leu Arg Gln Arg Gln Leu Asp
329          50          55          60
331 Gln Ala Asp Ala Val Leu Glu Pro Asp Ala Val Val Lys Arg Gln Glu
332          65          70          75          80
334 Ala Leu Ala Ala Ala Arg Leu Arg Met Gln Glu Asp Leu Asn Ala Gln
335          85          90          95
338 Val Glu Lys His Lys Glu Lys Leu Arg Gln Leu Glu Glu Glu Lys Arg
339          100          105          110
341 Arg Gln Lys Ile Glu Met Trp Asp Ser Met Gln Glu Gly Arg Ser Tyr
342          115          120          125
344 Arg Arg Asn Pro Gly Arg Pro Gln Glu Glu Asp Gly Pro Gly Pro Ser
345          130          135          140
347 Thr Ser Ser Ser Val Thr Arg Lys Gly Lys Ser Asp Lys Lys Pro Leu
348          145          150          155          160
350 Arg Gly Asn Gly Tyr Asn Pro Leu Thr Gly Glu Gly Gly Gly Thr Cys
351          165          170          175
353 Ala Trp Arg Pro Gly Arg Arg Gly Pro Ser Ser Gly Gly
354          180          185

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357 &lt;210&gt; SEQ ID NO: 5

358 &lt;211&gt; LENGTH: 1174

359 &lt;212&gt; TYPE: DNA

360 &lt;213&gt; ORGANISM: mammalian

362 &lt;220&gt; FEATURE:

363 &lt;221&gt; NAME/KEY: CDS

364 &lt;222&gt; LOCATION: (31)..(594)

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PATENT APPLICATION: US/10/039,050

DATE: 05/13/2002  
TIME: 16:48:29

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Output Set: N:\CRF3\05132002\J039050.raw

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/039,050

DATE: 05/13/2002

TIME: 16:48:29

Input Set : A:\PTO.DC.txt

Output Set: N:\CRF3\05132002\J039050.raw

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date



**Does Not Comply**  
**Corrected Diskette Needed**

OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/039,050

DATE: 05/07/2002

TIME: 10:04:45

Input Set : A:\12785.txt

Output Set: N:\CRF3\05072002\J039050.raw

4 <110> APPLICANT: Autogen Research Pty Ltd  
 6 <120> TITLE OF INVENTION: Novel genes and their use in the modulation of obesity,  
 diabetes  
 7 and energy imbalance  
 11 <130> FILE REFERENCE: 2309315/TDO  
 14 <140> CURRENT APPLICATION NUMBER: 10/039,050  
 C--> 15 <141> CURRENT FILING DATE: 2002-04-25  
 18 <150> PRIOR APPLICATION NUMBER: 60/141,441  
 19 <151> PRIOR FILING DATE: 1999-06-29  
 23 <160> NUMBER OF SEQ ID NOS: 22  
 26 <170> SOFTWARE: PatentIn Ver. 2.0

## ERRORED SEQUENCES

831 <210> SEQ ID NO: 22  
 832 <211> LENGTH: 18  
 833 <212> TYPE: PRT  
 834 <213> ORGANISM: mammalian  
 836 <400> SEQUENCE: 22  
 838 Arg Pro Gln Glu Glu Asp Gly Pro Gly Pro Ser Thr Ser Ser Ser Val  
 839 1 5 10 15  
 841 Thr Arg  
 E--> 845 ① -delete

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/039,050

DATE: 05/07/2002

TIME: 10:04:46

Input Set : A:\12785.txt

Output Set: N:\CRF3\05072002\J039050.raw

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:845 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:22